SUBSTITUTE FORM PTO-1449 (MODIFIED) U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE		
	Attorney Docket No.	50093/016001
	Serial No.	09/516,061
	Applicant	Venkat Gopalan et al.
INFORMATION DISCLOSURE STATEMENT BY APPLICANT (Use several sheets if necessary)	Filing Date	March 1, 2000
	Group	1652
(37 C.F.R. §1.98(b))	IDS Filed	April 3, 2003
	Customer No.	21559

OTHER DOCUMENTS (INCLUDING AUTHOR, TITLE, DATE, PLACE OF PUBLICATION)	
CM	AV Alm, et al, 1999, *Nature* 397 (6715); 176-180
CM	AW Andersen, et al. Identification of a region of genetic variability among Bacillus anthracis strains and related species. J. Bacteriol 178:377-84 (1996).
CM	AX Andersson, et al, 1998, *Nature* 396 (6706); 133-140
CM	AY Blattner, et al, 1997, *Science* 277 (5331); 1453-1474
CM	AZ Clark, et al, 1998, *Curr. Microbiol.* 36 (3); 158-163
CM	BA Cole, et al, 1998, *Nature* 393 (6685); 537-544
CM	BB Ferretti, et al., Complete genome sequence of an M1 strain of Streptococcus pyogenes. Proc Natl Acad Sci U S A 98:4658-63 (2001).
CM	BC Fleischmann, et al, 1995, *Science* 269 (5223); 496-512
CM	BD Fraser, et al, 1995, *Science* 270 (5235); 397-403
CM	BE Fraser, et al, 1997, *Nature* 390 (6660); 580-586
CM	BF Fraser, et al, 1998, *Science* 281 (5375); 375-388
CM	BG Fsihi, et al, 1996, *Microbiology* 142 (Pt. 11); 3147-3161
CM	BH Fujita, et al, 1990, *Gene* 93 (1); 73-78
CM	BI Heidelberg, et al., DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae. Nature 406:477-83 (2000).
CM	BJ Himmelreich, et al, 1996, *Nucl. Acids Res.* 24 (22); 4420-4449

EXAMINER C Blattner	DATE CONSIDERED 4/7/03

EXAMINER: Initial citation considered. Draw line through citation if not in conformance and not considered. Include copy of this form with the next communication to applicant.

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OTHER DOCUMENTS (INCLUDING AUTHOR, TITLE, DATE, PLACE OF PUBLICATION)

BK	Kalman, et al, 1999, *Nat. Genet.* 21 (4); 385-389
BL	Kunst, et al, 1997, *Nature* 390 (6657); 249-256
BM	Miyata, et al, 1993, *Nucl. Acids Res.* 21 (20); 4816-4823
BN	Morse and Schmidt, 1992, *Gene* 117 (1); 61-66
BO	Nelson, et al, 1999, *Nature* 399 (6734); 323-329
BP	Ogasawara, et al, 1992, *Mol. Microbiol.* 6 (5); 629-634
BQ	Parkhill, et al., Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491. Nature 404:502-6 (2000).
BR	Parkhill, et al., The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervariable sequences. Nature 403:665-8 (2000).
BS	Pasqual & Vioque, 1996, *Eur. J. Biochem.* 241 (1); 17-24
BT	Region from a *Bordetella pertussis* Tohama I sequence from Sanger center & MDS Contig 267. Accession No. NC_002928, July 5, 2002.
BU	Region from a *Clostridium difficile* 630 (epidemic type X) sequence from Sanger center Contig 975. Accession No. NC_002933, November 6, 2001
BV	Region from a *Corynebacterium diphtheriae* sequence from Sanger center Contig 390. Accession No. NC_002935, November 6, 2001.
BW	Region from a *Klebsiella pneumoniae* M6H 78578 sequence from Washington University Contig 632. Accession No. NC_002941, July 7, 1999.
BX	Region from a *Mycobacterium avium* 104 sequence from TIGR. Accession No. NC_002943, February 14, 2002.
BY	Region from a *Neisseria gonorrhoea* FA 1090 sequence from University of Oklahoma ACGT Contig 60. Accession No. NC_002946, September 28, 2000.
BZ	Region from a *Porphyromonas gingivalis* W83 sequence from TIGR & Forsyth Dental Center. Accession No. NC_002950, December 7, 2001.

EXAMINER	DATE CONSIDERED
[signature]	4/3/03

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	Attorney Docket No.	50093/016001
	Serial No.	09/516,061
	Applicant	Venkat Gopalan et al.
INFORMATION DISCLOSURE STATEMENT BY APPLICANT (Use several sheets if necessary)	Filing Date	March 1, 2000
	Group	1652
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	Customer No.	21559

		OTHER DOCUMENTS (INCLUDING AUTHOR, TITLE, DATE, PLACE OF PUBLICATION)
CM	CA	Region from a *Salmonella paratyphi* A ATCC 9150 sequence from Washington University. Accession No. NC_002963, July 7, 1999.
CM	CB	Region from a *Staphylococcus aureus* COL sequence from TIGR. Accession No. NC_002951, September 14, 2001.
CM	CC	Region from a *Staphylococcus aureus* NCTC sequence from University of Oklahoma ACGT Config 561. Accession No. NC_002954, December 4, 2001.
CM	CD	Region from a *Streptococcus mutans* UAB159 sequence from University of Oklahoma ACGT Contig 299. Accession No. NC_002956, December 14, 2001.
CM	CE	Redenbach, et al, 1996, *Mol. Microbiol.* 21 (1); 77-96
CM	CF	Skovgaard, 1990, *Gene* 93 (1); 27-34
duplicates CM	CG	Stephens, et al., Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis. Science 282:754-9 (1998).
CM	CH	~~Stephens, et al, 1998, *Science* 282 (5389); 754-759~~
CM	CI	Stover, et al., Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen. Nature 406:959-64 (2000).
CM	CJ	Suhan, et al, 1994, *J. Bact.* 176 (17); 5233-5243
CM	CK	Takami, et al, 1999, *Biosci. Biotechnol. Biochem.* 63 (6); 1134-1137
CM	CL	Tettelin et al., Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. Science 293:498 (2001).
CM	CM	Tomb, et al, 1997, *Nature* 388 (6642); 539-547

EXAMINER	DATE CONSIDERED
	4/30/05

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SUBSTITUTE FORM PTO-1449 (MODIFIED) U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE	Attorney Docket No.	50093/016001
	Serial No.	09/516,061
	Applicant	Venkat Gopalan et al.
INFORMATION DISCLOSURE STATEMENT BY APPLICANT (Use several sheets if necessary)	Filing Date	March 1, 2000
	Group	1652
(37 C.F.R. §1.98(b))	IDS Filed	October 11, 2002
	Customer No.	21559

	OTHER DOCUMENTS (INCLUDING AUTHOR, TITLE, DATE, PLACE OF PUBLICATION)
	Region from a *Streptococcus mutans* UAB159 sequence from University of Oklahoma ACGT Contig 299.
	Region from a *Klebsiella pneumoniae* M6H 78578 sequence from Washington University Contig 632.
	Region from a *Salmonella paratyphi* A ATCC 9150 sequence from Washington University.
	Region from a *Pseudomonas aeruginosa* PAO1 sequence from Pathogenesis & University of Washington Contig 54.
	Region from a *Corynebacterium diphtheriae* sequence from Sanger center Contig 390.
	Region from a *Chlamydia trachomatis* MoPn sequence from TIGR & Manitoba University.
	Region from a *Vibrio cholerae* serotype 01, Biotype El Tor, Strain N16961 sequence from TIGR.
	Region from a *Neisseria gonorrhoea* FA 1090 sequence from University of Oklahoma ACGT Contig 60.
	Region from a Neisseria meningitidis serogroup A Strain Z2491 sequence from Sanger center & Oxford University.
	Region from a *Streptococcus pyogenes* M1 sequence from University of Oklahoma ACGT Contig 7.
	Region from a *Bordetella pertussis* Tohama I sequence from Sanger center & MDS Contig 267.
	Region from a *Porphyromonas gingivalis* W83 sequence from TIGR & Forsyth Dental Center.
	Region from a *Streptococcus pneumoniae* Type 4 sequence from TIGR.
	Region from a *Clostridium difficile* 630 (epidemic type X) sequence from Sanger center Contig 975.
	Region from a *Camphylobacter jejuni* NCTC sequence from Sanger center & MDS.
	Region from a *Bacillus anthracis* Ames sequence from TIGR.
	Region from a *Mycobacterium avium* 104 sequence from TIGR.
	Region from a *Staphylococcus aureus* NCTC sequence from University of Oklahoma ACGT Contig 561.
	Region from a *Staphylococcus aureus* COL sequence from TIGR.

EXAMINER C Nolton	DATE CONSIDERED 4/3/08

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19